GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 16:37:09 ; Search time 7.16981 Seconds
                                             (without alignments)
                                             203.901 Million cell updates/sec

Title: US-10-074-694-5
Perfect score: 803
Sequence: 1 MANLERTPIAIKPDGVQRGL..........WFKPEELVDYKSCAHDWVYE 152

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 57320 seqs, 9617956 residues

Total number of hits satisfying chosen parameters: 57320

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   Pending_Patents_AA_New:*
        1: /cgn2_6/ptodata71/paa/PCT_NEW_COMB.pep:*
        2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
        3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
        4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
        5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
        6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
        7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
        8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result   Query
No.   Score Match Length DB   ID   Description
----- ----- ------------ --   --   -------

OM protein - protein search, using sw model

```
                        GenCore version 5.1.6
                        Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:           December 16, 2005, 16:32:00 ; Search time 392.906 Seconds
                                                 (without alignments)
                                                 534.625 Million cell updates/sec

Title:            US-10-074-694-5
Perfect score:    803
Sequence:         1 MANLERTFIAIKPDGVQRGL.........WFKPEELVDYKSCAHDWVYE 152

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         786I189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters:    7861189

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000
```

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

```
Database :      Pending_Patents_AA_Main:*

   1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
   2: /cgn2_6/ptodata/1/paa/US066_COMB.pep:*
   3: /cgn2_6/ptodata/1/paa/US073_COMB.pep:*
   4: /cgn2_6/ptodata/1/paa/US074_COMB.pep:*
   5: /cgn2_6/ptodata/1/paa/US075_COMB.pep:*
   6: /cgn2_6/ptodata/1/paa/US076_COMB.pep:*
   7: /cgn2_6/ptodata/1/paa/US077_COMB.pep:*
   8: /cgn2_6/ptodata/1/paa/US078_COMB.pep:*
   9: /cgn2_6/ptodata/1/paa/US079_COMB.pep:*
  10: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
  11: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
  12: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
  13: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
  14: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
  15: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
  16: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
  17: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
  18: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
  19: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
  20: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
  21: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
  22: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
  23: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
  24: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
  25: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
  26: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
  27: /cgn2_6/ptodata/1/paa/US097_COMB.pep:*
  28: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
  29: /cgn2_6/ptodata/1/paa/US099_COMB.pep:*
  30: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
  31: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
  32: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
  33: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
  34: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
  35: /cgn2_6/ptodata/1/paa/US105_COMB.pep:*
  36: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
  37: /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
  38: /cgn2_6/ptodata/1/paa/US108_COMB.pep:*
  39: /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
  40: /cgn2_6/ptodata/1/paa/US110_COMB.pep:*
  41: /cgn2_6/ptodata/1/paa/US111_COMB.pep:*
  42: /cgn2_6/ptodata/1/paa/US112_COMB.pep:*
  43: /cgn2_6/ptodata/1/paa/US114_COMB.pep:*
  44: /cgn2_6/ptodata/1/paa/US600_COMB.pep:*
  45: /cgn2_6/ptodata/1/paa/US601_COMB.pep:*
  46: /cgn2_6/ptodata/1/paa/US602_COMB.pep:*
  47: /cgn2_6/ptodata/1/paa/US603_COMB.pep:*
  48: /cgn2_6/ptodata/1/paa/US604_COMB.pep:*
  49: /cgn2_6/ptodata/1/paa/US605_COMB.pep:*
  50: /cgn2_6/ptodata/1/paa/US606_COMB.pep:*
  51: /cgn2_6/ptodata/1/paa/US607_COMB.pep:*
```